Amendments to the Claims

The current status of the claims is as follows:

1. (Currently Amended) A first hybridization assay probe for use in determining the presence of HPV Type 16 nucleic acid in a sample, said first probe comprising an oligonucleotide up to 100 bases in length and having a base region that is at least 70% complementary to an at least 10 contiguous base region present in a first nucleic acid target region selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, and SEQ ID NO:8, ~~SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35 and SEQ ID NO:36,~~ wherein said first probe forms a detectable probe:target duplex with said first target region under selective stringency hybridization conditions, and wherein said first probe does not form a detectable probe:non-target duplex with nucleic acid from HPV Type 18 ~~6, 11, 31, 33, 35, 39, 45, 51, 52 and/or 58~~ under said conditions.

2. (Currently Amended) A nucleic acid hybrid formed between said first probe and said first target region of claim 1.

3. (Canceled)

4. (Currently Amended) A kit comprising:

said probe of claim 1; and

a set of amplification oligonucleotides for use in amplifying HPV Type 16 nucleic acid in a sample, said set including first and second amplification oligonucleotides, wherein ~~each of~~ said first ~~and second~~ amplification ~~oligonucleotides~~ oligonucleotide is up to 100 bases in length and

has a base region that is at least 70% complementary to an at least 10 contiguous base region present in a nucleic acid target region selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, and SEQ ID NO:4, ~~SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95 and SEQ ID NO:96,~~ wherein said second amplification oligonucleotide is up to 100 bases in length and has a base region that is at least 70% complementary to an at least 10 contiguous base region present in a nucleic acid target region selected from the group consisting of SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87 and SEQ ID NO:88, and wherein at least one of said first and second amplification oligonucleotides optionally includes a base sequence that is recognized by an RNA polymerase.

5. (Currently Amended) A kit comprising:

said first probe of claim 1; and

a second hybridization assay probe for use in determining the presence of HPV Type 18 nucleic acid in a sample, said second probe comprising an oligonucleotide up to 100 bases in length and having a base region that is at least 70% complementary to an at least 10 contiguous base region present in a second nucleic acid target region selected from the group consisting of SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, and SEQ ID NO:48, ~~SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83 and SEQ ID NO:84,~~ wherein said second probe forms a detectable probe:target duplex with said second target region under said conditions, and wherein said second probe does not form a detectable probe:non-target

duplex with nucleic acid from HPV Type 16 ~~6, 11, 31, 33, 35, 39, 45, 51, 52 and/or 58~~ under said conditions.

6. (Canceled)

7. (Canceled)

8. (Currently Amended) The kit of claim 5 further comprising a helper probe, said helper probe comprising an oligonucleotide up to 100 bases in length and having a base region that is at least 70% complementary to an at least 10 contiguous base region present in a third nucleic acid target region selected from the group consisting of ~~SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120;~~ SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123; and SEQ ID NO:124, ~~SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127 and SEQ ID NO:128;~~ wherein said helper probe binds to said third region under said conditions, thereby facilitating hybridization of said second probe to said second target region.

9. (Canceled)

10. (Canceled)

11. (Withdrawn - Currently Amended) A method for determining the presence of HPV Type 16 nucleic acid in a sample, said method comprising the steps of:

providing to a sample said first probe of claim 1 under said conditions; and

determining whether said probe:target duplex has formed as an indication of the presence of HPV Type 16 nucleic acid in said sample.

12. (Canceled)

13. (Withdrawn - Currently Amended) The method of claim 11 further comprising providing to said sample a set of amplification oligonucleotides, said set including first and second amplification oligonucleotides, wherein ~~each of~~ said first ~~and second~~ amplification ~~oligonucleotides~~ oligonucleotide is up to 100 bases in length and has a base region that is at least 70% complementary to an at least 10 contiguous base region present in a nucleic acid target region selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3; and SEQ ID NO:4, ~~SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95 and SEQ ID NO:96,~~ wherein said second amplification oligonucleotide is up to 100 bases in length and has a base region that is at least 70% complementary to an at least 10 contiguous base region present in a nucleic acid target region selected from the group consisting of SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87 and SEQ ID NO:88, and wherein at least one of said first and second amplification oligonucleotides optionally includes a base sequence that is recognized by an RNA polymerase.

14. (Withdrawn - Currently Amended) The method of claim 11 further comprising providing to said sample a second hybridization assay probe for use in determining the presence of HPV Type 18 nucleic acid in a sample, said second probe comprising an oligonucleotide up to 100 bases in length and having a base region that is at least 70% complementary to an at least 10 contiguous base region present in a second nucleic acid target region selected from the group consisting of SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47; and SEQ ID NO:48, ~~SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77,~~

~~SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83 and SEQ ID NO:84,~~ wherein said second probe forms a detectable probe:target duplex with said second target region under said conditions, and wherein said second probe does not form a detectable probe:non-target duplex with nucleic acid from HPV Type 16 ~~6, 11, 31, 33, 35, 39, 45, 51, 52 and/or 58~~ under said conditions.

15. (Withdrawn - Currently Amended) The method of claim 14 further comprising providing to said sample a helper probe, said helper probe comprising an oligonucleotide up to 100 bases in length and having a base region that is at least 70% complementary to an at least 10 contiguous base region present in a third nucleic acid target region selected from the group consisting of ~~SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120,~~ SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123~~,~~ and SEQ ID NO:124, ~~SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127 and SEQ ID NO:128,~~ wherein said helper probe binds to said third region under said conditions, thereby facilitating hybridization of said second probe to said second target region.

Claims 16-19 (Canceled)